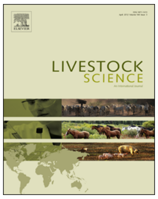
Livestock Science 176 (2015) 47–53

Contents lists available at ScienceDirect

Livestock Science

journal homepage: www.elsevier.com/locate/livsci



Comparing multi-trait Poisson and Gaussian Bayesian models for genetic evaluation of litter traits in pigs

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ARTICLE INFO

Article history:
Received 1 October 2014
Received in revised form
30 March 2015
Accepted 31 March 2015

Keywords:
Litter size
Count data
Multi-trait mixed models
MCMC

ABSTRACT

Reproductive traits as number of piglets born (NPB) and weaned (NWP) are directly related to the economic efficiency of swine production systems. Pig breeding programs seek to increase the number of weaned piglets per sow per year, and the NPB is among the factors that directly and indirectly influence the NWP. Thus, multi-trait evaluations are essential to estimate heritabilities and mainly genetic correlations between these traits over different farrowing orders. In general, Gaussian linear mixed models have been used to genetic evaluation of litter traits; however since these traits are characterized as count variables, Poisson models are also indicated. Some studies were carried out using Poisson mixed models in the area of Animal Breeding and Genetics, but they do not point out for a multi-trait scenario, as it should be for litter size at birth and weaning. Toward this orientation, we aimed to apply a multi-trait Poisson mixed model (MPM) for the genetic evaluation of the number of born and weaned piglets under a Bayesian framework. It was aimed also to compare the proposed model with the traditional multi-trait Gaussian model (MGM) by using posterior based goodness-of-fit measures. Two-trait analyses for NPB and NWP were performed separately by each considered farrowing order (first, second and third) using MPM and MGM fitted to data from a commercial Landrace population. Based on DIC (Deviance Information Criterion) and PMP (Posterior Model Probability) values, the MGM outperformed the MPM, but the genetic parameter and breeding values provided by both models were consistent and similar over the three first farrowing orders. Bayesian generalized a multi-trait mixed model approach is feasible for genetic evaluations in the animal breeding context and can be an alternative method for genetic evaluations assuming non-Normal phenotypes.

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http://dx.doi.org/10.1016/j.livsci.2015.03.030
1871-1413/

1. Introduction

Reproductive traits are directly related to the economic efficiency of swine production systems. The reproductive performance of animals is critical to efficiency and profitability in both breeding stock and commercial herds.

Pig breeding programs seek to increase the number of weaned piglets per sow per year (Imboonta et al., 2007), and the number of piglets born is among the factors that directly and indirectly influence the number of weaned piglets (Pires et al., 2000; Damgaard et al., 2003). Thus, genetic gains in litter size at weaning can be supported by selection strategies based on estimating genetic correlation with litter size at birth.

Historically, litter traits have mostly been evaluated using methodologies based on Gaussian linear mixed models (Holm et al., 2005; Serenius et al., 2008; Kapell et al., 2011). However, according to Foulley et al. (1987) and Tempelman and Gianola (1993), count reproductive traits such as litter size could be analyzed using a Poisson model, once the conditional distribution of embryo yield (in function of ovulation rate) is characterized as a Poisson process. Under these conditions, the authors found that the Poisson model led to better parameter estimates in comparison with a traditional Gaussian linear model. On the other hand, the Poisson model did not improve upon the Gaussian model in goodness of fit in a study of litter size in pigs (Perez-Enciso et al., 1993). Although these seminal studies have been extremely important to the dissemination of Poisson mixed models, they do not point out for analyses involving more than one trait. Thus, research developments related to the application and comparison of multi-trait Poisson mixed models for count traits, as litter size at birth and weaning, are justified and deserve attention in the field of animal breeding and genetics.

Since multi-trait Poisson mixed models are very complex to be fitted by the traditional REML method, Hadfield and Nakagawa (2010) proposed an alternative Bayesian approach via Markov chain Monte Carlo (MCMC) sampling based on the conditional probability distribution of latent variables, which in this case are the canonical parameters (mean) of the Poisson distributions. Under this viewpoint, other discrete distributions like Binomial, Geometric and zero-inflated Poisson (ZIP), among others, can be extended to the context of multi-trait mixed models. The authors applied these models to comparative biology analysis (phylogenies and taxonomies), in which the covariance matrix of random effects is named phylogenetic matrix. Thus, the replacement of this matrix by the traditional pedigree relationship matrix is presented as an alternative approach to fit generalized multi-trait mixed models in the field of quantitative genetics and animal breeding.

The present study aimed to apply a two-trait Poisson mixed model for the genetic evaluation of the number of born and weaned piglets from a Bayesian perspective. It was aimed also to compare the proposed model with the traditional multi-trait Gaussian model by using posterior based goodness-of-fit measures.

2. Material and methods

2.1. Data origin and structure

The data used in the present study originated from Landrace pigs produced by a farm located in the state of Santa Catarina, southern Brazil. The following traits were analyzed: number of born (NPB) and weaned (NWP) piglets in the first, second and third farrowing. No crossfostering technique was used in this farm. Usually, the crossfostering is applied to obtain litters with a similar number of piglets or with homogeneous weight, which increases the survival and weight gain of piglets until weaning (Bierhals et al., 2012). However, the use of this technique implies in unrealistic genetic parameters (heritabilities and genetic correlations) estimation for NPB and NWP (Roehe and Kennedy, 1995).

Fifteen contemporary groups were formed based on the year and the farrowing season, being groups with fewer than five observations removed from the database. Table 1 summarizes the total number of individuals, the mean and the coefficient of variation for the analyzed traits in each farrowing.

2.2. Statistical analysis

Two-trait analyses for NPB and NWP were performed separately by each farrowing using multi-trait Poisson (MPM) and Gaussian (MGM) models via MCMC Bayesian approach.

The MPM in (1) was implemented following the methodology proposed by Hadfield and Nakagawa (2010), which is based on the latent variable generalized linear mixed model given by

$$\boldsymbol{l} = X\boldsymbol{\beta} + \mathbf{Za} + \mathbf{e}, \qquad (1)$$

where $\boldsymbol{l}$ is the vector of a latent variable for each trait (NPB and NWP), which is introduced by means of the canonical parameter (often called the rate or mean parameter) of the Poisson distribution and the link function on the log scale, i.e., $y_{1i} \sim \mathrm{Poi}(\lambda_1 = \exp(l_{1i}))$and $y_{2i} \sim \mathrm{Poi}(\lambda_2 = \exp(l_{2i}))$, where $i=1,2,\ldots,N_j$, being N_j the number of observation for each trait j ($j=1$ and 2); exp is the inverse link function; and λ_1 and λ_2 are, respectively, the canonical parameter of the Poisson distribution for traits 1 (NPB) and 2 (NWP). Thus, the vector of latent variables assumes a multivariate normal distribution, $\boldsymbol{l}|\,\boldsymbol{\beta}, \mathbf{a}, \mathbf{G}_0, \mathbf{R}_0 \sim N(X\boldsymbol{\beta}+\mathbf{Za}, \mathbf{R}_0 \otimes \mathbf{I})$:

Table 1
Total number of individuals, the phenotypic mean and the coefficient of variation (CV) for the number of piglets born (NPB) and weaned (NWP) per farrowing orders (1, 2 and 3).

Farrowing	Traits	Number of individuals	Mean	CV (%)
First	NPB	557	10.59	22.78
	NWP	553	9.66	25.49
Second	NPB	422	10.68	26.05
	NWP	411	10.01	26.59
Third	NPB	348	11.22	23.79
	NWP	349	10.52	25.13